



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁵ : A61K 37/36, C12P 13/06, C12N 1/22, 15/18, 15/66, C07K 15/28	A1	(11) International Publication Number: WO 95/01802 (43) International Publication Date: 19 January 1995 (19.01.95)
(21) International Application Number: PCT/US94/07799 (22) International Filing Date: 8 July 1994 (08.07.94) (30) Priority Data: 08/089,670 9 July 1993 (09.07.93) US (71) Applicant (for all designated States except US): THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE [US/US]; 720 Rutland Avenue, Baltimore, MD 21205 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): LEE, Se-Jin [US/US]; 6711 Chokeberry Road, Baltimore, MD 21209 (US). HUYNH, Thanh [US/US]; 5100 South Bend Road, Baltimore, MD 21209 (US). (74) Agents: WETHERELL, John, R. et al.; Spensley Horn Jubas & Lubitz, 5th floor, 1880 Century Park East, Los Angeles, CA 90067 (US).	(81) Designated States: AU, CA, JP, US, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i>	
(54) Title: GROWTH DIFFERENTIATION FACTOR-7 (57) Abstract Growth differentiation factor-7 (GDF-7) is disclosed along with its polynucleotide sequence and amino acid sequence. Also disclosed are diagnostic and therapeutic methods of using the GDF-7 polypeptide and polynucleotide sequences.		

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GROWTH DIFFERENTIATION FACTOR-7

BACKGROUND OF THE INVENTION

1. *Field of the Invention*

The invention relates generally to growth factors and specifically to a new member of the transforming growth factor beta (TGF- β) superfamily, which is denoted, growth differentiation factor-7 (GDF-7).

2. *Description of Related Art*

The transforming growth factor β (TGF- β) superfamily encompasses a group of structurally-related proteins which affect a wide range of differentiation processes during embryonic development. The family includes, Mullerian inhibiting substance (MIS), which is required for normal male sex development (Behringer, *et al.*, *Nature*, 345:167, 1990), *Drosophila* decapentaplegic (DPP) gene product, which is required for dorsal-ventral axis formation and morphogenesis of the imaginal disks (Padgett, *et al.*, *Nature*, 325:81-84, 1987), the *Xenopus* Vg-1 gene product, which localizes to the vegetal pole of eggs ((Weeks, *et al.*, *Cell*, 51:861-867, 1987), the activins (Mason, *et al.*, *Biochem, Biophys. Res. Commun.*, 135:957-964, 1986), which can induce the formation of mesoderm and anterior structures in *Xenopus* embryos (Thomsen, *et al.*, *Cell*, 63:485, 1990), and the bone morphogenetic proteins (BMPs, osteogenin, OP-1) which can induce *de novo* cartilage and bone formation (Sampath, *et al.*, *J. Biol. Chem.*, 265:13198, 1990). The TGF- β s can influence a variety of differentiation processes, including adipogenesis, myogenesis, chondrogenesis, hematopoiesis, and epithelial cell differentiation (for review, see Massague, *Cell* 49:437, 1987).

The proteins of the TGF- β family are initially synthesized as a large precursor protein which subsequently undergoes proteolytic cleavage at a cluster of basic residues approximately 110-140 amino acids from the C-terminus. The C-terminal regions, or mature regions, of the proteins are all structurally related and the different family members can be classified into distinct subgroups based on the extent of their homology. Although the homologies within particular subgroups range from 70% to 90% amino acid sequence identity, the homologies between subgroups are significantly lower, generally ranging from only 20% to 50%. In each case, the active species appears to be a disulfide-linked dimer of C-terminal fragments. Studies have shown that when the pro-region of a member of the TGF- β family is coexpressed with a mature region of another member of the TGF- β family, intracellular dimerization and secretion of biologically active homodimers occur (Gray, A., and Maston, A., *Science*, 247:1328, 1990). Additional studies by Hammonds, *et al.*, (*Molec. Endocrin.* 5:149, 1991) showed that the use of the BMP-2 pro-region combined with the BMP-4 mature region led to dramatically improved expression of mature BMP-4. For most of the family members that have been studied, the homodimeric species has been found to be biologically active, but for other family members, like the inhibins (Ling, *et al.*, *Nature*, 321:779, 1986) and the TGF- β s (Cheifetz, *et al.*, *Cell*, 48:409, 1987), heterodimers have also been detected, and these appear to have different biological properties than the respective homodimers.

Identification of new factors that are tissue-specific in their expression pattern will provide a greater understanding of that tissue's development and function.

SUMMARY OF THE INVENTION

The present invention provides a cell growth and differentiation factor, GDF-7, a polynucleotide sequence which encodes the factor, and antibodies which are immunoreactive with the factor. This factor appears to relate to various cell proliferative disorders, especially those involving neural tissue.

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Thus, in one embodiment, the invention provides a method for detecting a cell proliferative disorder of neural origin and which is associated with GDF-7. In another embodiment, the invention provides a method for treating a cell proliferative disorder by suppressing or enhancing GDF-7 activity.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGURE 1 shows RNase protection assays detecting expression of GDF-7 mRNA in neural tissue and cell lines. The arrow denotes the position of the protected species.

5 FIGURE 2 shows nucleotide and predicted amino acid sequences of murine GDF-7. The putative pentabasic processing sites in the murine sequence is boxed.

10 FIGURE 3 shows the alignment of the C-terminal sequences of GDF-7 with other members of the TGF- β superfamily. The conserved cysteine residues are boxed. Dashes denote gaps introduced in order to maximize alignment.

15 FIGURE 4 shows amino acid homologies among different members of the TGF- β superfamily. Numbers represent percent amino acid identities between each pair calculated from the first conserved cysteine to the C-terminus. Boxes represent homologies among highly-related members within particular subgroups.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides a growth and differentiation factor, GDF-7 and a polynucleotide sequence encoding GDF-7. GDF-7 is expressed in neural tissue. In one embodiment, the invention provides a method for detection of a cell proliferative disorder of neural origin which is associated with GDF-7 expression. In another embodiment, the invention provides a method for treating a cell proliferative disorder by using an agent which suppresses or enhances GDF-7 activity.

The TGF- β superfamily consists of multifunctional polypeptides that control proliferation, differentiation, and other functions in many cell types. Many of the peptides have regulatory, both positive and negative, effects on other peptide growth factors. The structural homology between the GDF-7 protein of this invention and the members of the TGF- β family, indicates that GDF-7 is a new member of the family of growth and differentiation factors. Based on the known activities of many of the other members, it can be expected that GDF-7 will also possess biological activities that will make it useful as a diagnostic and therapeutic reagent.

In particular, certain members of this superfamily have expression patterns or possess activities that relate to the function of the nervous system. For example, one family member, namely GDNF, has been shown to be a potent neurotrophic factor that can promote the survival of dopaminergic neurons (Lin, *et al.*, *Science*, 260:1130). Another family member, namely dorsalin, is capable of promoting the differentiation of neural crest cells (Baster, *et al.*, *Cell*, 73:687). The inhibins and activins have been shown to be expressed in the brain (Meunier, *et al.*, *Proc. Natl. Acad. Sci., USA*, 85:247, 1988; Sawchenko, *et al.*, *Nature*, 334:615, 1988), and activin has been shown to be capable of functioning as a nerve cell survival molecule (Schubert, *et al.*, *Nature*, 344:868,

- 1990). Another family member, namely, GDF-1, is nervous system-specific in its expression pattern (Lee, *Proc. Natl. Acad. Sci., USA*, 88:4250, 1991), and certain other family members, such as Vgr-1 (Lyons, *et al., Proc. Natl. Acad. Sci., USA*, 86:4554, 1989; Jones, *et al., Development*, 111:531, 1991), OP-1 (Ozkaynak, *et al., J. Biol. Chem.*, 267:25220, 1992), and BMP-4 (Jones, *et al., Development*, 111:531, 1991), are also known to be expressed in the nervous system. By analogy GDF-7 may have applications in the treatment of neurodegenerative diseases or in maintaining cells or tissues in culture prior to transplantation.
- 10 Several members of the TGF- β superfamily possess activities suggesting possible applications for the treatment of cell proliferative disorders, such as cancer. In particular, TGF- β has been shown to be potent growth inhibitor for a variety of cell types (Massague, *Cell*, 49:437, 1987), MIS has been shown to inhibit the growth of human endometrial carcinoma tumors in nude mice (Donahoe, *et al., Ann. Surg.*, 194:472, 1981), and inhibin α has been shown to suppress the development of tumors both in the ovary and in the testis (Matzuk, *et al., Nature*, 360:313, 1992). GDF-7 may have a similar activity and may therefore be useful as an anti-proliferative agent, such as for the treatment of tumors of neural origin.
- 20 Many of the members of the TGF- β family are also important mediators of tissue repair. TGF- β has been shown to have marked effects on the formation of collagen and causes of striking angiogenic response in the newborn mouse (Roberts, *et al., Proc. Natl. Acad. Sci., USA*, 83:4167, 1986). the BMP's can induce new bone growth and are effective for the treatment of fractures and other skeletal defects (Glowacki, *et al., Lancet*, 1:959, 1981; Ferguson, *et al., Clin. Orthoped. Relat. Res.*, 227:265, 1988; Johnson, *et al., Clin Orthoped. Relat. Res.*, 230:257, 1988). GDF-7 may have similar activities and may be useful in repair of tissue injury caused by trauma or burns for example.
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The term "substantially pure" as used herein refers to GDF-7 which is substantially free of other proteins, lipids, carbohydrates or other materials with which it is naturally associated. One skilled in the art can purify GDF-7 using standard techniques for protein purification. The substantially pure polypeptide
5 will yield a single major band on a non-reducing polyacrylamide gel. The purity of the GDF-7 polypeptide can also be determined by amino-terminal amino acid sequence analysis. GDF-7 polypeptide includes functional fragments of the polypeptide, as long as the activity of GDF-7 remains. Smaller peptides containing the biological activity of GDF-7 are included in the invention.

10 The invention provides polynucleotides encoding the GDF-7 protein. These polynucleotides include DNA, cDNA and RNA sequences which encode GDF-7. It is understood that all polynucleotides encoding all or a portion of GDF-7 are also included herein, as long as they encode a polypeptide with GDF-7 activity. Such polynucleotides include naturally occurring, synthetic, and intentionally
15 manipulated polynucleotides. For example, GDF-7 polynucleotide may be subjected to site-directed mutagenesis. The polynucleotide sequence for GDF-7 also includes antisense sequences. The polynucleotides of the invention include sequences that are degenerate as a result of the genetic code. There are 20 natural amino acids, most of which are specified by more than one
20 codon. Therefore, all degenerate nucleotide sequences are included in the invention as long as the amino acid sequence of GDF-7 polypeptide encoded by the nucleotide sequence is functionally unchanged.

Specifically disclosed herein is a genomic DNA sequence containing a portion of the GDF-7 gene. The sequence contains an open reading frame
25 corresponding to the predicted C-terminal region of the GDF-7 precursor protein. The encoded polypeptide is predicted to contain a potential pentabasic proteolytic processing site. Cleavage of the precursor at this

site would generate a mature biologically active C-terminal fragment of 146 amino acids with a predicted molecular weight of approximately 14,900.

5 The C-terminal region of GDF-7 following the putative proteolytic processing site shows significant homology to the known members of the TGF- β superfamily. The GDF-7 sequence contains most of the residues that are highly conserved in other family members (see Figure 3). Among the known family members, GDF-7 is most homologous to BMP-2 and BMP-4 (57% sequence identity) (see Figure 4).

10 Minor modifications of the recombinant GDF-7 primary amino acid sequence may result in proteins which have substantially equivalent activity as compared to the GDF-7 polypeptide described herein. Such modifications may be deliberate, as by site-directed mutagenesis, or may be spontaneous. All of the polypeptides produced by these modifications are included herein as long as the biological activity of GDF-7 still exists. Further, deletion of one or more
15 amino acids can also result in a modification of the structure of the resultant molecule without significantly altering its biological activity. This can lead to the development of a smaller active molecule which would have broader utility. For example, one can remove amino or carboxy terminal amino acids which are not required for GDF-7 biological activity.

20 The nucleotide sequence encoding the GDF-7 polypeptide of the invention includes the disclosed sequence and conservative variations thereof. The term "conservative variation" as used herein denotes the replacement of an amino acid residue by another, biologically similar residue. Examples of conservative variations include the substitution of one hydrophobic residue such as
25 isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as the substitution of arginine for lysine, glutamic for aspartic acid, or glutamine for asparagine, and the like. The term

"conservative variation" also includes the use of a substituted amino acid in place of an unsubstituted parent amino acid provided that antibodies raised to the substituted polypeptide also immunoreact with the unsubstituted polypeptide.

5 DNA sequences of the invention can be obtained by several methods. For example, the DNA can be isolated using hybridization techniques which are well known in the art. These include, but are not limited to: 1) hybridization of genomic or cDNA libraries with probes to detect homologous nucleotide sequences, 2) polymerase chain reaction (PCR) on genomic DNA or cDNA
10 using primers capable of annealing to the DNA sequence of interest, and 3) antibody screening of expression libraries to detect cloned DNA fragments with shared structural features.

Preferably the GDF-7 polynucleotide of the invention is derived from a mammalian organism, and most preferably from a mouse, rat, or human.
15 Screening procedures which rely on nucleic acid hybridization make it possible to isolate any gene sequence from any organism, provided the appropriate probe is available. Oligonucleotide probes, which correspond to a part of the sequence encoding the protein in question, can be synthesized chemically. This requires that short, oligopeptide stretches of amino acid sequence must
20 be known. The DNA sequence encoding the protein can be deduced from the genetic code, however, the degeneracy of the code must be taken into account. It is possible to perform a mixed addition reaction when the sequence is degenerate. This includes a heterogeneous mixture of denatured double-stranded DNA. For such screening, hybridization is preferably
25 performed on either single-stranded DNA or denatured double-stranded DNA. Hybridization is particularly useful in the detection of cDNA clones derived from sources where an extremely low amount of mRNA sequences relating to the polypeptide of interest are present. In other words, by using stringent

hybridization conditions directed to avoid non-specific binding, it is possible, for example, to allow the autoradiographic visualization of a specific cDNA clone by the hybridization of the target DNA to that single probe in the mixture which is its complete complement (Wallace, *et al.*, *Nucl. Acid Res.*, 9:879, 1981).

The development of specific DNA sequences encoding GDF-7 can also be obtained by: 1) isolation of double-stranded DNA sequences from the genomic DNA; 2) chemical manufacture of a DNA sequence to provide the necessary codons for the polypeptide of interest; and 3) *in vitro* synthesis of a double-stranded DNA sequence by reverse transcription of mRNA isolated from a eukaryotic donor cell. In the latter case, a double-stranded DNA complement of mRNA is eventually formed which is generally referred to as cDNA.

Of the three above-noted methods for developing specific DNA sequences for use in recombinant procedures, the isolation of genomic DNA isolates is the least common. This is especially true when it is desirable to obtain the microbial expression of mammalian polypeptides due to the presence of introns.

The synthesis of DNA sequences is frequently the method of choice when the entire sequence of amino acid residues of the desired polypeptide product is known. When the entire sequence of amino acid residues of the desired polypeptide is not known, the direct synthesis of DNA sequences is not possible and the method of choice is the synthesis of cDNA sequences. Among the standard procedures for isolating cDNA sequences of interest is the formation of plasmid- or phage-carrying cDNA libraries which are derived from reverse transcription of mRNA which is abundant in donor cells that have a high level of genetic expression. When used in combination with polymerase chain reaction technology, even rare expression products can be cloned. In

those cases where significant portions of the amino acid sequence of the polypeptide are known, the production of labeled single or double-stranded DNA or RNA probe sequences duplicating a sequence putatively present in the target cDNA may be employed in DNA/DNA hybridization procedures which are
5 carried out on cloned copies of the cDNA which have been denatured into a single-stranded form (Jay, *et al.*, *Nucl. Acid Res.*, 11:2325, 1983).

A cDNA expression library, such as lambda gt11, can be screened indirectly for GDF-7 peptides having at least one epitope, using antibodies specific for GDF-7. Such antibodies can be either polyclonally or monoclonally derived
10 and used to detect expression product indicative of the presence of GDF-7 cDNA.

DNA sequences encoding GDF-7 can be expressed *in vitro* by DNA transfer into a suitable host cell. "Host cells" are cells in which a vector can be propagated and its DNA expressed. The term also includes any progeny of
15 the subject host cell. It is understood that all progeny may not be identical to the parental cell since there may be mutations that occur during replication. However, such progeny are included when the term "host cell" is used. Methods of stable transfer, meaning that the foreign DNA is continuously maintained in the host, are known in the art.

20 In the present invention, the GDF-7 polynucleotide sequences may be inserted into a recombinant expression vector. The term "recombinant expression vector" refers to a plasmid, virus or other vehicle known in the art that has been manipulated by insertion or incorporation of the GDF-7 genetic sequences. Such expression vectors contain a promoter sequence which
25 facilitates the efficient transcription of the inserted genetic sequence of the host. The expression vector typically contains an origin of replication, a promoter, as well as specific genes which allow phenotypic selection of the transformed

cells. Vectors suitable for use in the present invention include, but are not limited to the T7-based expression vector for expression in bacteria (Rosenberg, *et al.*, *Gene*, 56:125, 1987), the pMSXND expression vector for expression in mammalian cells (Lee and Nathans, *J. Biol. Chem.*, 263:3521, 1988) and baculovirus-derived vectors for expression in insect cells. The DNA segment can be present in the vector operably linked to regulatory elements, for example, a promoter (e.g., T7, metallothionein I, or polyhedrin promoters).

Polynucleotide sequences encoding GDF-7 can be expressed in either prokaryotes or eukaryotes. Hosts can include microbial, yeast, insect and mammalian organisms. Methods of expressing DNA sequences having eukaryotic or viral sequences in prokaryotes are well known in the art. Biologically functional viral and plasmid DNA vectors capable of expression and replication in a host are known in the art. Such vectors are used to incorporate DNA sequences of the invention. Preferably, the mature C-terminal region of GDF-7 is expressed from a cDNA clone containing the entire coding sequence of GDF-7. Alternatively, the C-terminal portion of GDF-7 can be expressed as a fusion protein with the pro- region of another member of the TGF- β family or co-expressed with another pro- region (see for example, Hammonds, *et al.*, *Molec. Endocrin.* 5:149, 1991; Gray, A., and Mason, A., *Science*, 247:1328, 1990).

Transformation of a host cell with recombinant DNA may be carried out by conventional techniques as are well known to those skilled in the art. Where the host is prokaryotic, such as *E. coli*, competent cells which are capable of DNA uptake can be prepared from cells harvested after exponential growth phase and subsequently treated by the CaCl_2 method using procedures well known in the art. Alternatively, MgCl_2 or RbCl can be used. Transformation can also be performed after forming a protoplast of the host cell if desired.

When the host is a eukaryote, such methods of transfection of DNA as calcium phosphate co-precipitates, conventional mechanical procedures such as microinjection, electroporation, insertion of a plasmid encased in liposomes, or virus vectors may be used. Eukaryotic cells can also be cotransformed with

5 DNA sequences encoding the GDF-7 of the invention, and a second foreign DNA molecule encoding a selectable phenotype, such as the herpes simplex thymidine kinase gene. Another method is to use a eukaryotic viral vector, such as simian virus 40 (SV40) or bovine papilloma virus, to transiently infect or transform eukaryotic cells and express the protein. (see for example,

10 *Eukaryotic Viral Vectors*, Cold Spring Harbor Laboratory, Gluzman ed., 1982).

Isolation and purification of microbial expressed polypeptide, or fragments thereof, provided by the invention, may be carried out by conventional means including preparative chromatography and immunological separations involving monoclonal or polyclonal antibodies.

15 The invention includes antibodies immunoreactive with GDF-7 polypeptide or functional fragments thereof. Antibody which consists essentially of pooled monoclonal antibodies with different epitopic specificities, as well as distinct monoclonal antibody preparations are provided. Monoclonal antibodies are made from antigen containing fragments of the protein by methods well known

20 to those skilled in the art (Kohler, *et al.*, *Nature*, 256:495, 1975). The term antibody as used in this invention is meant to include intact molecules as well as fragments thereof, such as Fab and F(ab')₂, which are capable of binding an epitopic determinant on GDF-7.

The term "cell-proliferative disorder" denotes malignant as well as non-malignant

25 cell populations which often appear to differ from the surrounding tissue both morphologically and genotypically. Malignant cells (i.e. cancer) develop as a result of a multistep process. The GDF-7 polynucleotide that is an antisense

molecule is useful in treating malignancies of the various organ systems, particularly, for example, cells in neural tissue. Essentially, any disorder which is etiologically linked to altered expression of GDF-7 could be considered susceptible to treatment with a GDF-7 suppressing reagent. One such disorder is a malignant cell proliferative disorder, for example.

The invention provides a method for detecting a cell proliferative disorder of neural tissue which comprises contacting an anti-GDF-7 antibody with a cell suspected of having a GDF-7 associated disorder and detecting binding to the antibody. The antibody reactive with GDF-7 is labeled with a compound which allows detection of binding to GDF-7. For purposes of the invention, an antibody specific for GDF-7 polypeptide may be used to detect the level of GDF-7 in biological fluids and tissues. Any specimen containing a detectable amount of antigen can be used. A preferred sample of this invention is neural tissue. The level of GDF-7 in the suspect cell can be compared with the level in a normal cell to determine whether the subject has a GDF-7-associated cell proliferative disorder. Preferably the subject is human.

The antibodies of the invention can be used in any subject in which it is desirable to administer *in vitro* or *in vivo* immunodiagnosis or immunotherapy. The antibodies of the invention are suited for use, for example, in immunoassays in which they can be utilized in liquid phase or bound to a solid phase carrier. In addition, the antibodies in these immunoassays can be detectably labeled in various ways. Examples of types of immunoassays which can utilize antibodies of the invention are competitive and non-competitive immunoassays in either a direct or indirect format. Examples of such immunoassays are the radioimmunoassay (RIA) and the sandwich (immunometric) assay. Detection of the antigens using the antibodies of the invention can be done utilizing immunoassays which are run in either the forward, reverse, or simultaneous modes, including immunohistochemical assays on physiological samples.

Those of skill in the art will know, or can readily discern, other immunoassay formats without undue experimentation.

5 The antibodies of the invention can be bound to many different carriers and used to detect the presence of an antigen comprising the polypeptide of the invention. Examples of well-known carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, agaroses and magnetite. The nature of the carrier can be either soluble or insoluble for purposes of the invention. Those skilled in the art will know of other suitable carriers for binding antibodies, or will be
10 able to ascertain such, using routine experimentation.

There are many different labels and methods of labeling known to those of ordinary skill in the art. Examples of the types of labels which can be used in the present invention include enzymes, radioisotopes, fluorescent compounds, colloidal metals, chemiluminescent compounds, phosphorescent compounds,
15 and bioluminescent compounds. Those of ordinary skill in the art will know of other suitable labels for binding to the antibody, or will be able to ascertain such, using routine experimentation.

Another technique which may also result in greater sensitivity consists of coupling the antibodies to low molecular weight haptens. These haptens can
20 then be specifically detected by means of a second reaction. For example, it is common to use such haptens as biotin, which reacts with avidin, or dinitrophenyl, puridoxal, and fluorescein, which can react with specific anti-hapten antibodies.

In using the monoclonal antibodies of the invention for the *in vivo* detection of
25 antigen, the detectably labeled antibody is given a dose which is diagnostically effective. The term "diagnostically effective" means that the amount of

detectably labeled monoclonal antibody is administered in sufficient quantity to enable detection of the site having the antigen comprising a polypeptide of the invention for which the monoclonal antibodies are specific.

5 The concentration of detectably labeled monoclonal antibody which is administered should be sufficient such that the binding to those cells having the polypeptide is detectable compared to the background. Further, it is desirable that the detectably labeled monoclonal antibody be rapidly cleared from the circulatory system in order to give the best target-to-background signal ratio.

10 As a rule, the dosage of detectably labeled monoclonal antibody for *in vivo* diagnosis will vary depending on such factors as age, sex, and extent of disease of the individual. Such dosages may vary, for example, depending on whether multiple injections are given, antigenic burden, and other factors known to those of skill in the art.

15 For *in vivo* diagnostic imaging, the type of detection instrument available is a major factor in selecting a given radioisotope. The radioisotope chosen must have a type of decay which is detectable for a given type of instrument. Still another important factor in selecting a radioisotope for *in vivo* diagnosis is that deleterious radiation with respect to the host is minimized. Ideally, a radio-
20 isotope used for *in vivo* imaging will lack a particle emission, but produce a large number of photons in the 140-250 keV range, which may readily be detected by conventional gamma cameras.

For *in vivo* diagnosis radioisotopes may be bound to immunoglobulin either directly or indirectly by using an intermediate functional group. Intermediate
25 functional groups which often are used to bind radioisotopes which exist as metallic ions to immunoglobulins are the bifunctional chelating agents such as

diethylenetriaminepentacetic acid (DTPA) and ethylenediaminetetraacetic acid (EDTA) and similar molecules. Typical examples of metallic ions which can be bound to the monoclonal antibodies of the invention are ^{111}In , ^{97}Ru , ^{67}Ga , ^{68}Ga , ^{72}As , ^{89}Zr , and ^{201}Tl .

- 5 The monoclonal antibodies of the invention can also be labeled with a paramagnetic isotope for purposes of *in vivo* diagnosis, as in magnetic resonance imaging (MRI) or electron spin resonance (ESR). In general, any conventional method for visualizing diagnostic imaging can be utilized. Usually gamma and positron emitting radioisotopes are used for camera imaging and
- 10 paramagnetic isotopes for MRI. Elements which are particularly useful in such techniques include ^{157}Gd , ^{55}Mn , ^{162}Dy , ^{52}Cr , and ^{56}Fe .

The monoclonal antibodies of the invention can be used *in vitro* and *in vivo* to monitor the course of amelioration of a GDF-7-associated disease in a subject. Thus, for example, by measuring the increase or decrease in the number of

15 cells expressing antigen comprising a polypeptide of the invention or changes in the concentration of such antigen present in various body fluids, it would be possible to determine whether a particular therapeutic regimen aimed at ameliorating the GDF-7-associated disease is effective. The term "ameliorate" denotes a lessening of the detrimental effect of the GDF-7-associated disease

20 in the subject receiving therapy.

The present invention identifies a nucleotide sequence that can be expressed in an altered manner as compared to expression in a normal cell, therefore it is possible to design appropriate therapeutic or diagnostic techniques directed to this sequence. Thus, where a cell-proliferative disorder is associated with

25 the expression of GDF-7, nucleic acid sequences that interfere with GDF-7 expression at the translational level can be used. This approach utilizes, for example, antisense nucleic acid and ribozymes to block translation of a specific

GDF-7 mRNA, either by masking that mRNA with an antisense nucleic acid or by cleaving it with a ribozyme.

Antisense nucleic acids are DNA or RNA molecules that are complementary to at least a portion of a specific mRNA molecule (Weintraub, *Scientific American*, 5 262:40, 1990). In the cell, the antisense nucleic acids hybridize to the corresponding mRNA, forming a double-stranded molecule. The antisense nucleic acids interfere with the translation of the mRNA, since the cell will not translate a mRNA that is double-stranded. Antisense oligomers of about 15 nucleotides are preferred, since they are easily synthesized and are less likely to cause problems than larger molecules when introduced into the target GDF-10 7-producing cell. The use of antisense methods to inhibit the *in vitro* translation of genes is well known in the art (Marcus-Sakura, *Anal.Biochem.*, 172:289, 1988).

Ribozymes are RNA molecules possessing the ability to specifically cleave 15 other single-stranded RNA in a manner analogous to DNA restriction endonucleases. Through the modification of nucleotide sequences which encode these RNAs, it is possible to engineer molecules that recognize specific nucleotide sequences in an RNA molecule and cleave it (Cech, *J.Amer.Med. Assn.*, 260:3030, 1988). A major advantage of this approach is that, because 20 they are sequence-specific, only mRNAs with particular sequences are inactivated.

There are two basic types of ribozymes namely, *tetrahymena*-type (Hasselhoff, *Nature*, 334:585, 1988) and "hammerhead"-type. *Tetrahymena*-type ribozymes recognize sequences which are four bases in length, while "hammerhead"-type 25 ribozymes recognize base sequences 11-18 bases in length. The longer the recognition sequence, the greater the likelihood that the sequence will occur exclusively in the target mRNA species. Consequently, hammerhead-type

ribozymes are preferable to *tetrahymena*-type ribozymes for inactivating a specific mRNA species and 18-based recognition sequences are preferable to shorter recognition sequences.

5 The present invention also provides gene therapy for the treatment of cell proliferative or immunologic disorders which are mediated by GDF-7 protein. Such therapy would achieve its therapeutic effect by introduction of the GDF-7 antisense polynucleotide into cells having the proliferative disorder. Delivery of antisense GDF-7 polynucleotide can be achieved using a recombinant expression vector such as a chimeric virus or a colloidal dispersion system.
10 Especially preferred for therapeutic delivery of antisense sequences is the use of targeted liposomes.

Various viral vectors which can be utilized for gene therapy as taught herein include adenovirus, herpes virus, vaccinia, or, preferably, an RNA virus such as a retrovirus. Preferably, the retroviral vector is a derivative of a murine or
15 avian retrovirus. Examples of retroviral vectors in which a single foreign gene can be inserted include, but are not limited to: Moloney murine leukemia virus (MoMuLV), Harvey murine sarcoma virus (HaMuSV), murine mammary tumor virus (MuMTV), and Rous Sarcoma Virus (RSV). A number of additional retroviral vectors can incorporate multiple genes. All of these vectors can
20 transfer or incorporate a gene for a selectable marker so that transduced cells can be identified and generated. By inserting a GDF-7 sequence of interest into the viral vector, along with another gene which encodes the ligand for a receptor on a specific target cell, for example, the vector is now target specific. Retroviral vectors can be made target specific by inserting, for example, a
25 polynucleotide encoding a sugar, a glycolipid, or a protein. Preferred targeting is accomplished by using an antibody to target the retroviral vector. Those of skill in the art will know of, or can readily ascertain without undue experimentation, specific polynucleotide sequences which can be inserted into the retroviral

genome to allow target specific delivery of the retroviral vector containing the GDF-7 antisense polynucleotide.

- Since recombinant retroviruses are defective, they require assistance in order to produce infectious vector particles. This assistance can be provided, for example, by using helper cell lines that contain plasmids encoding all of the structural genes of the retrovirus under the control of regulatory sequences within the LTR. These plasmids are missing a nucleotide sequence which enables the packaging mechanism to recognize an RNA transcript for encapsidation. Helper cell lines which have deletions of the packaging signal include, but are not limited to ψ 2, PA317 and PA12, for example. These cell lines produce empty virions, since no genome is packaged. If a retroviral vector is introduced into such cells in which the packaging signal is intact, but the structural genes are replaced by other genes of interest, the vector can be packaged and vector virion produced.
- Alternatively, NIH 3T3 or other tissue culture cells can be directly transfected with plasmids encoding the retroviral structural genes *gag*, *pol* and *env*, by conventional calcium phosphate transfection. These cells are then transfected with the vector plasmid containing the genes of interest. The resulting cells release the retroviral vector into the culture medium.
- Another targeted delivery system for GDF-7 antisense polynucleotides is a colloidal dispersion system. Colloidal dispersion systems include macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. The preferred colloidal system of this invention is a liposome. Liposomes are artificial membrane vesicles which are useful as delivery vehicles *in vitro* and *in vivo*. It has been shown that large unilamellar vesicles (LUV), which range in size from 0.2-4.0 μ m can encapsulate a substantial percentage of an

aqueous buffer containing large macromolecules. RNA, DNA and intact virions can be encapsulated within the aqueous interior and be delivered to cells in a biologically active form (Fraley, et al., *Trends Biochem. Sci.*, 6:77, 1981). In addition to mammalian cells, liposomes have been used for delivery of

5 polynucleotides in plant, yeast and bacterial cells. In order for a liposome to be an efficient gene transfer vehicle, the following characteristics should be present: (1) encapsulation of the genes of interest at high efficiency while not compromising their biological activity; (2) preferential and substantial binding to a target cell in comparison to non-target cells; (3) delivery of the aqueous

10 contents of the vesicle to the target cell cytoplasm at high efficiency; and (4) accurate and effective expression of genetic information (Mannino, et al., *Biotechniques*, 6:682, 1988).

The composition of the liposome is usually a combination of phospholipids, particularly high-phase-transition-temperature phospholipids, usually in

15 combination with steroids, especially cholesterol. Other phospholipids or other lipids may also be used. The physical characteristics of liposomes depend on pH, ionic strength, and the presence of divalent cations.

Examples of lipids useful in liposome production include phosphatidyl compounds, such as phosphatidylglycerol, phosphatidylcholine,

20 phosphatidylserine, phosphatidylethanolamine, sphingolipids, cerebroside, and gangliosides. Particularly useful are diacylphosphatidylglycerols, where the lipid moiety contains from 14-18 carbon atoms, particularly from 16-18 carbon atoms, and is saturated. Illustrative phospholipids include egg phosphatidylcholine, dipalmitoylphosphatidylcholine and distearoylphosphatidylcholine.

25 The targeting of liposomes can be classified based on anatomical and mechanistic factors. Anatomical classification is based on the level of selectivity, for example, organ-specific, cell-specific, and organelle-specific.

Mechanistic targeting can be distinguished based upon whether it is passive or active. Passive targeting utilizes the natural tendency of liposomes to distribute to cells of the reticulo-endothelial system (RES) in organs which contain sinusoidal capillaries. Active targeting, on the other hand, involves alteration of the liposome by coupling the liposome to a specific ligand such as a monoclonal antibody, sugar, glycolipid, or protein, or by changing the composition or size of the liposome in order to achieve targeting to organs and cell types other than the naturally occurring sites of localization.

The surface of the targeted delivery system may be modified in a variety of ways. In the case of a liposomal targeted delivery system, lipid groups can be incorporated into the lipid bilayer of the liposome in order to maintain the targeting ligand in stable association with the liposomal bilayer. Various linking groups can be used for joining the lipid chains to the targeting ligand.

Due to the expression of GDF-7 in neural tissue, there are a variety of applications using the polypeptide, polynucleotide, and antibodies of the invention, related to this tissue. Such applications include treatment of cell proliferative disorders involving this tissue. In addition, GDF-7 may be useful in various gene therapy procedures.

The following examples are intended to illustrate but not limit the invention. While they are typical of those that might be used, other procedures known to those skilled in the art may alternatively be used.

EXAMPLE 1
IDENTIFICATION AND ISOLATION OF A NOVEL
TGF- β FAMILY MEMBER

To identify a new member of the TGF- β superfamily, degenerate
5 oligonucleotides were designed which corresponded to two conserved regions
among the known family members: one region spanning the two tryptophan
residues conserved in all family members except MIS and the other region
spanning the invariant cysteine residues near the C-terminus. These primers
were used for polymerase chain reactions on mouse genomic DNA followed
10 by subcloning the PCR products using restriction sites placed at the 5' ends
of the primers, picking individual *E. coli* colonies carrying these subcloned
inserts, and using a combination of random sequencing and hybridization
analysis to eliminate known members of the superfamily.

GDF-7 was identified from a mixture of PCR products obtained with the primers
15 SJL141: 5'-CCGGAATTCGGITGG(G/C/A)A(G/A/T/C)(A/G)A(T/C)TGG(A/G)TI
(A/G)TI(T/G)CICC-3' (SEQ ID NO:1)
SJL146: 5'CCGGAATTC(G/A)CAI(G/C)C(G/A)CAIG(C/A)(G/A/T/C)C(G/T)IACI
(G/A)(T/C)CAT-3' (SEQ ID NO:2)

PCR using these primers was carried out with 2 μ g mouse genomic DNA at
20 94°C for 1 min, 50°C for 2 min, and 72°C for 2 min for 40 cycles.

PCR products of approximately 280 bp were gel-purified, digested with Eco RI,
gel-purified again, and subcloned in the Bluescript vector (Stratagene, San
Diego, CA). Bacterial colonies carrying individual subclones were picked into
96 well microtiter plates, and multiple replicas were prepared by plating the
25 cells onto nitrocellulose. The replicate filters were hybridized to probes

representing known members of the family, and DNA was prepared from non-hybridizing colonies for sequence analysis.

5 The primer combination of SJL141 and SJL146, encoding the amino acid sequences GW(H/Q/N/K/D/E)(D/N)W(V/I/M)(V/I/M)(A/S)P (SEQ ID NO:3) and M(V/I/M/T/A)V(R/S)(A/S)C(G/A)C (SEQ ID NO:4), respectively, yielded five previously identified sequences (BMP-2, BMP-4, inhibin β B, GDF-3 and GDF-5) and one novel sequence, which was designated GDF-7, among 147 subclones analyzed.

EXAMPLE 2

10 EXPRESSION PATTERN AND SEQUENCE OF GDF-7

To determine the expression pattern of GDF-7, RNA samples prepared from a variety of tissues were screened by Northern analysis and RNase protection. As shown in Figure 1, GDF-7 mRNA was detected in fetal and neonatal brain and in the Neuro 2A neuroblastoma cell line.

15 To obtain a larger segment of the GDF-7 gene, a mouse genomic library was screened with a probe derived from the GDF-7 PCR product. The partial sequence of a GDF-7 genomic clone is shown in Figure 2a. The sequence contains an open reading frame corresponding to the predicted C-terminal region of the GDF-7 precursor protein. The predicted GDF-7 sequence
20 contains a potential proteolytic processing site, which is boxed. Cleavage of the precursor at this site would generate a mature C-terminal fragment 146 amino acids in length with a predicted molecular weight of 14,900.

The C-terminal region of GDF-7 following the putative proteolytic processing site shows significant homology to the known members of the TGF- β
25 superfamily (Figure 3). Figure 3 shows the alignment of the C-terminal sequences of GDF-7 with the corresponding regions of human GDF-1 (Lee,

Proc. Natl. Acad. Sci. USA, 88:4250-4254, 1991), human BMP-2 and 4 (Wozney, *et al.*, *Science*, 242:1528-1534, 1988), human Vgr-1 (Celeste, *et al.*, *Proc. Natl. Acad. Sci. USA*, 87:9843-9847, 1990), human OP-1 (Ozkaynak, *et al.*, *EMBO J.*, 9:2085-2093, 1990), human BMP-5 (Celeste, *et al.*, *Proc. Natl. Acad. Sci. USA*, 87:9843-9847, 1990), human BMP-3 (Wozney, *et al.*, *Science*, 242:1528-1534, 1988), human MIS (Cate, *et al.*, *Cell*, 45:685-698, 1986), human inhibin alpha, β A, and β B (Mason, *et al.*, *Biochem. Biophys. Res. Commun.*, 135:957-964, 1986), human TGF- β 1 (Derynck, *et al.*, *Nature*, 316:701-705, 1985), human TGF- β 2 (deMartin, *et al.*, *EMBO J.*, 6:3673-3677, 1987), and human TGF- β 3 (ten Dijke, *et al.*, *Proc. Natl. Acad. Sci. USA*, 85:4715-4719, 1988). The conserved cysteine residues are boxed. Dashes denote gaps introduced in order to maximize the alignment.

GDF-7 contains most of the residues that are highly conserved in other family members, including the seven cysteine residues with their characteristic spacing.

FIGURE 4 shows the amino acid homologies among the different members of the TGF- β superfamily. Numbers represent percent amino acid identities between each pair calculated from the first conserved cysteine to the C-terminus. Boxes represent homologies among highly-related members within particular subgroups. In this region, GDF-7 is most homologous to BMP-2 and BMP-4 (57% sequence identity).

Although the invention has been described with reference to the presently preferred embodiment, it should be understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims.

SUMMARY OF SEQUENCES

SEQ ID NO: 1 is the nucleotide sequence for the GDF-7 primer, SJL141.

SEQ ID NO: 2 is the nucleotide sequence for the GDF-7 primer, SJL146.

SEQ ID NO: 3 is the amino acid sequence for the GDF-7 primer, SJL141.

5 SEQ ID NO: 4 is the amino acid sequence for the GDF-7 primer, SJL146.

SEQ ID NO: 5 is the nucleotide and deduced amino acid sequence for the GDF-7.

SEQ ID NO: 6 is the amino acid sequence for the GDF-7.

SEQ ID NO: 7 is the amino acid sequence for the C-terminal end of GDF-7.

10 SEQ ID NO: 8 is the amino acid sequence for the C-terminal end of GDF-1.

SEQ ID NO: 9 is the amino acid sequence for the C-terminal end of BMP-2.

SEQ ID NO: 10 is the amino acid sequence for the C-terminal end of BMP-4.

SEQ ID NO: 11 is the amino acid sequence for the C-terminal end of Vgr-1.

SEQ ID NO: 12 is the amino acid sequence for the C-terminal end of OP-1.

15 SEQ ID NO: 13 is the amino acid sequence for the C-terminal end of BMP-5.

SEQ ID NO: 14 is the amino acid sequence for the C-terminal end of BMP-3.

SEQ ID NO: 15 is the amino acid sequence for the C-terminal end of MIS.

SEQ ID NO: 16 is the amino acid sequence for the C-terminal end of Inhibin-alpha.

5 SEQ ID NO: 17 is the amino acid sequence for the C-terminal end of Inhibin-beta-alpha.

SEQ ID NO: 18 is the amino acid sequence for the C-terminal end of Inhibin-beta-beta.

SEQ ID NO: 19 is the amino acid sequence for the C-terminal end of TGF-beta-1.

10 SEQ ID NO: 20 is the amino acid sequence for the C-terminal end of TGF-beta-2.

SEQ ID NO: 21 is the amino acid sequence for the C-terminal end of TGF-beta-3.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

(ii) TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7

5 (iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Spensley Horn Jubas & Lubitz
(B) STREET: 1880 Century Park East, Suite 500
10 (C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 90067

(v) COMPUTER READABLE FORM:

15 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

20 (A) APPLICATION NUMBER: PCT
(B) FILING DATE: 08-JUL-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

25 (A) NAME: TUMARKIN, LISA A., PH.D.
(B) REGISTRATION NUMBER: P-38,347
(C) REFERENCE/DOCKET NUMBER: FD-2348

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (619) 455-5100
(B) TELEFAX: (619) 455-5110

30 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:
(B) CLONE: SJL141

5

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..35
(D) OTHER INFORMATION: /note= "R=adenine or guanine;
S-cytosine or guanine; M=adenine or cytosine;
N=adenine, cytosine, guanine or thymine;
K=thymine or guanine; B=inosine"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGGAATTTCG GBTGGVANRA YTGGRBTBRTB KCBCC

35

15 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:
(B) CLONE: SJL146

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..33
(D) OTHER INFORMATION: /note= "R=adenine or guanine;
S=cytosine or guanine; M=adenine or cytosine;
N=adenine, cytosine, guanine or thymine;
Y=cytosine or thymine; K=thymine or guanine;
B=inosine"

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCGGAATTCTC CABSCRCABG MNCKBACBRY CAT

33

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

10 (vii) IMMEDIATE SOURCE:

(B) CLONE: SJL141

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION: 1..9
15 (D) OTHER INFORMATION: /note= "His=His, Gln, Asn, Lys, Asp
or Glu; Asp=Asp or Asn; Val=Val, Ile or Met;
Ala=Ala or Ser"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20 Gly Trp His Asp Trp Val Val Ala Pro
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: SJL146

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..8

(D) OTHER INFORMATION: /note= "Val, position 1=Val, Ile, Met, Th:

5 or

Ala; Arg=Arg or Ser; Ala=Ala or Ser; Gly=Gly or
Ala"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Val Arg Ala Cys Gly Cys
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 519 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: GDF-7

20 (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 34..516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTGCAGAGC CGCCACCGGT ACCAGGACCA GGC GCT GGG TCA CGC AAA GCC AAC 54
Ala Gly Ser Arg Lys Ala Asn
1 5

CTG GGC GGT CGC AGG CGG CGG CGG ACT GCG CTG GCT GGG ACT CGG GGA 102
Leu Gly Gly Arg Arg Arg Arg Arg Thr Ala Leu Ala Gly Thr Arg Gly
10 15 20

	GGC CAG GGA AGC GGT GGT GGC GGC GGT GGC GGT GGC GGC GGC GGC GGC	150
	Ala Gln Gly Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly	
	25 30 35	
5	GGC GGC GGC GGC GGC GGC GGC GGC GCA GGC AGG GGC CAC GGG CGC AGA	198
	Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Gly Arg Gly His Gly Arg Arg	
	40 45 50 55	
	GGC CGG AGC CGC TGC AGT CGC AAG TCA CTG CAC GTG GAC TTT AAG GAG	246
	Gly Arg Ser Arg Cys Ser Arg Lys Ser Leu His Val Asp Phe Lys Glu	
	60 65 70	
10	CTG GGC TGG GAC GAC TGG ATC ATC GCG CCA TTA GAC TAC GAG GCA TAC	294
	Leu Gly Trp Asp Asp Trp Ile Ile Ala Pro Leu Asp Tyr Glu Ala Tyr	
	75 80 85	
	CAC TGC GAG GGC GTT TGC GAC TTT CCT CTG CGC TCG CAC CTG GAG CCT	342
	His Cys Glu Gly Val Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro	
15	90 95 100	
	ACC AAC CAC GCC ATC ATT CAG ACG CTG CTC AAC TCC ATG GCG CCC GAC	390
	Thr Asn His Ala Ile Ile Gln Thr Leu Leu Asn Ser Met Ala Pro Asp	
	105 110 115	
20	GCT GCG CCA GCC TCC TGC TGC GTG CCC GCA AGG CTC AGT CCC ATC AGC	438
	Ala Ala Pro Ala Ser Cys Cys Val Pro Ala Arg Leu Ser Pro Ile Ser	
	120 125 130 135	
	ATT CTC TAC ATC GAT GCC GCC AAC AAC GTG GTC TAC AAG CAG TAC GAA	486
	Ile Leu Tyr Ile Asp Ala Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu	
	140 145 150	
25	GAC ATG GTG GTG GAG GCC TGC GGC TGC AGG TAG	519
	Asp Met Val Val Glu Ala Cys Gly Cys Arg	
	155 160	

(2) INFORMATION FOR SEQ ID NO:6:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

-33-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Gly Ser Arg Lys Ala Asn Leu Gly Gly Arg Arg Arg Arg Arg Thr
 1 5 10 15
 Ala Leu Ala Gly Thr Arg Gly Ala Gln Gly Ser Gly Gly Gly Gly Gly
 5 20 25 30
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala
 35 40 45
 Gly Arg Gly His Gly Arg Arg Gly Arg Ser Arg Cys Ser Arg Lys Ser
 50 55 60
 10 Leu His Val Asp Phe Lys Glu Leu Gly Trp Asp Asp Trp Ile Ile Ala
 65 70 75 80
 Pro Leu Asp Tyr Glu Ala Tyr His Cys Glu Gly Val Cys Asp Phe Pro
 85 90 95
 Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Ile Ile Gln Thr Leu
 15 100 105 110
 Leu Asn Ser Met Ala Pro Asp Ala Ala Pro Ala Ser Cys Cys Val Pro
 115 120 125
 Ala Arg Leu Ser Pro Ile Ser Ile Leu Tyr Ile Asp Ala Ala Asn Asn
 130 135 140
 20 Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val Glu Ala Cys Gly Cys
 145 150 155 160
 Arg

(2) INFORMATION FOR SEQ ID NO:7:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
(B) CLONE: GDF-7

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..119

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	Gly	Gly	Gly	Gly	Gly	Ala	Gly	Arg	Gly	His	Gly	Arg	Arg	Gly	Arg	Ser	
	1				5					10				15			
	Arg	Cys	Ser	Arg	Lys	Ser	Leu	His	Val	Asp	Phe	Lys	Glu	Leu	Gly	Trp	
10				20					25					30			
	Asp	Asp	Trp	Ile	Ile	Ala	Pro	Leu	Asp	Tyr	Glu	Ala	Tyr	His	Cys	Glu	
			35					40					45				
	Gly	Val	Cys	Asp	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His	
		50						55				60					
15	Ala	Ile	Ile	Gln	Thr	Leu	Leu	Asn	Ser	Met	Ala	Pro	Asp	Ala	Ala	Pro	
	65					70					75					80	
	Ala	Ser	Cys	Cys	Val	Pro	Ala	Arg	Leu	Ser	Pro	Ile	Ser	Ile	Leu	Tyr	
					85					90					95		
	Ile	Asp	Ala	Ala	Asn	Asn	Val	Val	Tyr	Lys	Gln	Tyr	Glu	Asp	Met	Val	
20				100					105					110			
	Val	Glu	Ala	Cys	Gly	Cys	Arg										
					115												

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: GDF-1

(ix) FEATURE:

(A) NAME/KEY: Peptide

5

(B) LOCATION: 1..123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

	Arg	Pro	Arg	Arg	Asp	Ala	Glu	Pro	Val	Leu	Gly	Gly	Gly	Pro	Gly	Gly	
	1				5					10					15		
	Ala	Cys	Arg	Ala	Arg	Arg	Leu	Tyr	Val	Ser	Phe	Arg	Glu	Val	Gly	Trp	
10				20					25					30			
	His	Arg	Trp	Val	Ile	Ala	Pro	Arg	Gly	Phe	Leu	Ala	Asn	Tyr	Cys	Gln	
			35					40					45				
	Gly	Gln	Cys	Ala	Leu	Pro	Val	Ala	Leu	Ser	Gly	Ser	Gly	Gly	Pro	Pro	
		50					55					60					
15	Ala	Leu	Asn	His	Ala	Val	Leu	Arg	Ala	Leu	Met	His	Ala	Ala	Ala	Pro	
	65					70					75					80	
	Gly	Ala	Ala	Asp	Leu	Pro	Cys	Cys	Val	Pro	Ala	Arg	Leu	Ser	Pro	Ile	
				85						90					95		
	Ser	Val	Leu	Phe	Phe	Asp	Asn	Ser	Asp	Asn	Val	Val	Leu	Arg	Gln	Tyr	
20				100					105					110			
	Glu	Asp	Met	Val	Val	Asp	Glu	Cys	Gly	Cys	Arg						
				115					120								

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
(B) CLONE: BMP-2

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..118

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

	Arg	Glu	Lys	Arg	Gln	Ala	Lys	His	Lys	Gln	Arg	Lys	Arg	Leu	Lys	Ser	
	1				5					10					15		
	Ser	Cys	Lys	Arg	His	Pro	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	
10				20					25					30			
	Asn	Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	His	Ala	Phe	Tyr	Cys	His	
			35					40					45				
	Gly	Glu	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	
		50					55					60					
15	Ala	Ile	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Lys	Ile	Pro	Lys	
	65					70					75				80		
	Ala	Cys	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	
					85					90				95			
	Asp	Glu	Asn	Glu	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Asp	Met	Val	Val	
20				100					105					110			
	Glu	Gly	Cys	Gly	Cys	Arg											
				115													

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: BMP-4

(ix) FEATURE:

(A) NAME/KEY: Protein

5

(B) LOCATION: 1..118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

	Lys	Arg	Ser	Pro	Lys	His	His	Ser	Gln	Arg	Ala	Arg	Lys	Lys	Asn	Lys	
	1				5				10					15			
10	Asn	Cys	Arg	Arg	His	Ser	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	
				20					25					30			
	Asn	Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	Gln	Ala	Phe	Tyr	Cys	His	
			35					40					45				
	Gly	Asp	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	
		50					55					60					
15	Ala	Ile	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Ser	Ile	Pro	Lys	
	65					70				75					80		
	Ala	Cys	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	
					85					90					95		
	Asp	Glu	Tyr	Asp	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Glu	Met	Val	Val	
20				100					105					110			
	Glu	Gly	Cys	Gly	Cys	Arg											
				115													

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: Vgr-1

(ix) FEATURE:

(A) NAME/KEY: Protein

5

(B) LOCATION: 1..119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

	Ser	Arg	Gly	Ser	Gly	Ser	Ser	Asp	Tyr	Asn	Gly	Ser	Glu	Leu	Lys	Thr	
	1				5					10					15		
10	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	Asp	Leu	Gly	Trp	
				20					25					30			
	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Gly	Tyr	Ala	Ala	Asn	Tyr	Cys	Asp	
			35					40					45				
	Gly	Glu	Cys	Ser	Phe	Pro	Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His	
		50					55					60					
15	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Leu	Met	Asn	Pro	Glu	Tyr	Val	Pro	
	65					70					75					80	
	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	
				85						90					95		
	Phe	Asp	Asp	Asn	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val	
20				100					105						110		
	Val	Arg	Ala	Cys	Gly	Cys	His										
				115													

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
(B) CLONE: OP-1

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..119

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln	
	1				5					10				15			
	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp	
10				20					25					30			
	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Tyr	Tyr	Cys	Glu	
			35					40					45				
	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala	Thr	Asn	His	
		50					55					60					
15	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val	Pro	
	65					70					75					80	
	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	
				85						90					95		
	Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val	
20				100					105					110			
	Val	Arg	Ala	Cys	Gly	Cys	His										
				115													

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: BMP-5

(ix) FEATURE:

(A) NAME/KEY: Protein

5

(B) LOCATION: 1..119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

	Ser	Arg	Met	Ser	Ser	Val	Gly	Asp	Tyr	Asn	Thr	Ser	Glu	Gln	Lys	Gln	
	1				5					10					15		
10	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp	
				20					25					30			
	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Phe	Tyr	Cys	Asp	
			35					40					45				
	Gly	Glu	Cys	Ser	Phe	Pro	Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His	
		50					55					60					
15	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Leu	Met	Phe	Pro	Asp	His	Val	Pro	
	65					70					75					80	
	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	
					85					90					95		
	Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val	
20				100					105					110			
	Val	Arg	Ser	Cys	Gly	Cys	His										
					115												

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
(B) CLONE: BMP-3

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..120

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

	Glu	Gln	Thr	Leu	Lys	Lys	Ala	Arg	Arg	Lys	Gln	Trp	Ile	Glu	Pro	Arg	
	1				5					10					15		
10	Asn	Cys	Ala	Arg	Arg	Tyr	Leu	Lys	Val	Asp	Phe	Ala	Asp	Ile	Gly	Trp	
				20					25					30			
	Ser	Glu	Trp	Ile	Ile	Ser	Pro	Lys	Ser	Phe	Asp	Ala	Tyr	Tyr	Cys	Ser	
			35					40					45				
	Gly	Ala	Cys	Gln	Phe	Pro	Met	Pro	Lys	Ser	Leu	Lys	Pro	Ser	Asn	His	
		50					55					60					
15	Ala	Thr	Ile	Gln	Ser	Ile	Val	Arg	Ala	Val	Gly	Val	Val	Pro	Gly	Ile	
	65					70					75				80		
	Pro	Glu	Pro	Cys	Cys	Val	Pro	Glu	Lys	Met	Ser	Ser	Leu	Ser	Ile	Leu	
					85					90					95		
20	Phe	Phe	Asp	Glu	Asn	Lys	Asn	Val	Val	Leu	Lys	Val	Tyr	Pro	Asn	Met	
				100					105					110			
	Thr	Val	Glu	Ser	Cys	Ala	Cys	Arg									
					115			120									

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: MIS

(ix) FEATURE:

(A) NAME/KEY: Protein

5

(B) LOCATION: 1..116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

	Gly	Pro	Gly	Arg	Ala	Gln	Arg	Ser	Ala	Gly	Ala	Thr	Ala	Ala	Asp	Gly	
	1				5					10					15		
	Pro	Cys	Ala	Leu	Arg	Glu	Leu	Ser	Val	Asp	Leu	Arg	Ala	Glu	Arg	Ser	
10				20					25					30			
	Val	Leu	Ile	Pro	Glu	Thr	Tyr	Gln	Ala	Asn	Asn	Cys	Gln	Gly	Val	Cys	
			35					40					45				
	Gly	Trp	Pro	Gln	Ser	Asp	Arg	Asn	Pro	Arg	Tyr	Gly	Asn	His	Val	Val	
		50					55					60					
15	Leu	Leu	Leu	Lys	Met	Gln	Ala	Arg	Gly	Ala	Ala	Leu	Ala	Arg	Pro	Pro	
	65					70					75				80		
	Cys	Cys	Val	Pro	Thr	Ala	Tyr	Ala	Gly	Lys	Leu	Leu	Ile	Ser	Leu	Ser	
					85					90					95		
	Glu	Glu	Arg	Ile	Ser	Ala	His	His	Val	Pro	Asn	Met	Val	Ala	Thr	Glu	
20				100					105					110			
	Cys	Gly	Cys	Arg													
				115													

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:
(B) CLONE: Inhibin-alpha

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..122

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

	Ala	Leu	Arg	Leu	Leu	Gln	Arg	Pro	Pro	Glu	Glu	Pro	Ala	Ala	His	Ala
	1				5					10					15	
	Asn	Cys	His	Arg	Val	Ala	Leu	Asn	Ile	Ser	Phe	Gln	Glu	Leu	Gly	Trp
10				20					25					30		
	Glu	Arg	Trp	Ile	Val	Tyr	Pro	Pro	Ser	Phe	Ile	Phe	His	Tyr	Cys	His
			35					40					45			
	Gly	Gly	Cys	Gly	Leu	His	Ile	Pro	Pro	Asn	Leu	Ser	Leu	Pro	Val	Pro
		50					55					60				
15	Gly	Ala	Pro	Pro	Thr	Pro	Ala	Gln	Pro	Tyr	Ser	Leu	Leu	Pro	Gly	Ala
	65					70					75				80	
	Gln	Pro	Cys	Cys	Ala	Ala	Leu	Pro	Gly	Thr	Met	Arg	Pro	Leu	His	Val
					85					90					95	
	Arg	Thr	Thr	Ser	Asp	Gly	Gly	Tyr	Ser	Phe	Lys	Tyr	Glu	Thr	Val	Pro
20					100				105					110		
	Asn	Leu	Leu	Thr	Gln	His	Cys	Ala	Cys	Ile						
					115				120							

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: Inhibin-beta-alpha

(ix) FEATURE:

(A) NAME/KEY: Protein

5 (B) LOCATION: 1..122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

His Arg Arg Arg Arg Arg Gly Leu Glu Cys Asp Gly Lys Val Asn Ile
 1 5 10 15
 Cys Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn
 10 20 25 30
 Asp Trp Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Glu Gly
 35 40 45
 Glu Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe
 50 55 60
 15 His Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe
 65 70 75 80
 Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser
 85 90 95
 20 Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln
 100 105 110
 Asn Met Ile Val Glu Glu Cys Gly Cys Ser
 115 120

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 121 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

-45-

(vii) IMMEDIATE SOURCE:

(B) CLONE: Inhibin-beta-beta

(ix) FEATURE:

(A) NAME/KEY: Protein

5

(B) LOCATION: 1..121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

	His	Arg	Ile	Arg	Lys	Arg	Gly	Leu	Glu	Cys	Asp	Gly	Arg	Thr	Asn	Leu	
	1				5					10					15		
10	Cys	Cys	Arg	Gln	Gln	Phe	Phe	Ile	Asp	Phe	Arg	Leu	Ile	Gly	Trp	Asn	
				20					25					30			
	Asp	Trp	Ile	Ile	Ala	Pro	Thr	Gly	Tyr	Tyr	Gly	Asn	Tyr	Cys	Glu	Gly	
			35					40					45				
	Ser	Cys	Pro	Ala	Tyr	Leu	Ala	Gly	Val	Pro	Gly	Ser	Ala	Ser	Ser	Phe	
		50					55					60					
15	His	Thr	Ala	Val	Val	Asn	Gln	Tyr	Arg	Met	Arg	Gly	Leu	Asn	Pro	Gly	
	65					70				75					80		
	Thr	Val	Asn	Ser	Cys	Cys	Ile	Pro	Thr	Lys	Leu	Ser	Thr	Met	Ser	Met	
				85						90					95		
	Leu	Tyr	Phe	Asp	Asp	Glu	Tyr	Asn	Ile	Val	Lys	Arg	Asp	Val	Pro	Asn	
20				100				105						110			
	Met	Ile	Val	Glu	Glu	Cys	Gly	Cys	Ala								
				115				120									

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

-46-

(vii) IMMEDIATE SOURCE:

(B) CLONE: TGF-beta-1

(ix) FEATURE:

(A) NAME/KEY: Protein

5

(B) LOCATION: 1..115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

	His	Arg	Arg	Ala	Leu	Asp	Thr	Asn	Tyr	Cys	Phe	Ser	Ser	Thr	Glu	Lys	
	1				5					10					15		
10	Asn	Cys	Cys	Val	Arg	Gln	Leu	Tyr	Ile	Asp	Phe	Arg	Lys	Asp	Leu	Gly	
				20					25					30			
	Trp	Lys	Trp	Ile	His	Glu	Pro	Lys	Gly	Tyr	His	Ala	Asn	Phe	Cys	Leu	
				35					40					45			
	Gly	Pro	Cys	Pro	Tyr	Ile	Trp	Ser	Leu	Asp	Thr	Gln	Tyr	Ser	Lys	Val	
		50					55					60					
15	Leu	Ala	Leu	Tyr	Asn	Gln	His	Asn	Pro	Gly	Ala	Ser	Ala	Ala	Pro	Cys	
	65					70					75					80	
	Cys	Val	Pro	Gln	Ala	Leu	Glu	Pro	Leu	Pro	Ile	Val	Tyr	Tyr	Val	Gly	
				85						90					95		
	Arg	Lys	Pro	Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	Arg	Ser	Cys	
20				100					105					110			
	Lys	Cys	Ser														
				115													

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

-47-

(vii) IMMEDIATE SOURCE:

(B) CLONE: TGF-beta-2

(ix) FEATURE:

(A) NAME/KEY: Protein

5 (B) LOCATION: 1..115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys Lys Arg Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp
 1 5 10 15
 Asn Cys Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly
 10 20 25 30
 Trp Lys Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala
 35 40 45
 Gly Ala Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val
 50 55 60
 15 Leu Ser Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys
 65 70 75 80
 Cys Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly
 85 90 95
 20 Lys Thr Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys
 100 105 110
 Lys Cys Ser
 115

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: TGF-beta-3

(ix) FEATURE:

(A) NAME/KEY: Protein

5

(B) LOCATION: 1..115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Lys Lys Arg Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu
1 5 10 15

10

Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly
20 25 30

Trp Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser
35 40 45

Gly Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val
50 55 60

15

Leu Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys
65 70 75 80

Cys Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly
85 90 95

20

Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys
100 105 110

Lys Cys Ser
115

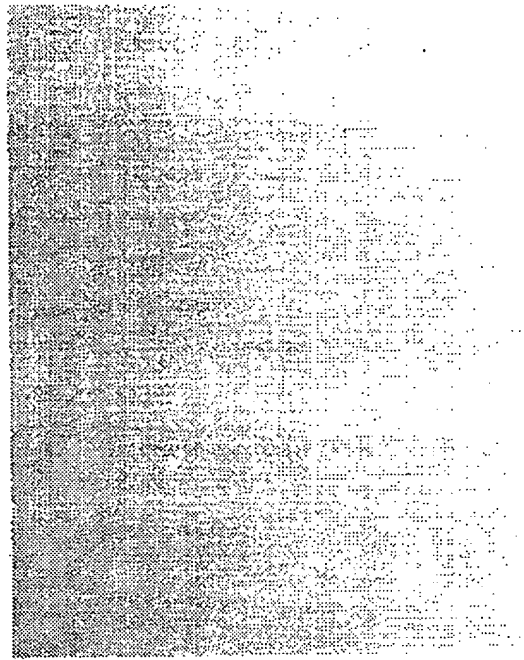
CLAIMS

1. Substantially pure growth differentiation factor-7 (GDF-7) and functional fragments thereof.
2. An isolated polynucleotide sequence encoding the GDF-7 polypeptide of claim 1.
3. The polynucleotide sequence of claim 2, wherein the polynucleotide is isolated from a mammalian cell.
4. The polynucleotide of claim 3, wherein the mammalian cell is selected from the group consisting of mouse, rat, and human cell.
5. An expression vector including the polynucleotide of claim 2.
6. The vector of claim 5, wherein the vector is a plasmid.
7. The vector of claim 5, wherein the vector is a virus.
8. A host cell stably transformed with the vector of claim 5.
9. The host cell of claim 8, wherein the cell is prokaryotic.
10. The host cell of claim 8, wherein the cell is eukaryotic.
11. Antibodies reactive with the polypeptide of claim 1 or fragments thereof.
12. The antibodies of claim 11, wherein the antibodies are polyclonal.

13. The antibodies of claim 11, wherein the antibodies are monoclonal.
14. A method of detecting a cell proliferative disorder comprising contacting the antibody of claim 11 with a specimen of a subject suspected of having a GDF-7 associated disorder and detecting binding of the antibody.
15. The method of claim 14, wherein the cell is a neural cell.
16. The method of claim 14, wherein the detecting is *in vivo*.
17. The method of claim 16, wherein the antibody is detectably labeled.
18. The method of claim 17, wherein the detectable label is selected from the group consisting of a radioisotope, a fluorescent compound, a bioluminescent compound and a chemiluminescent compound.
19. The method of claim 14, wherein the detection is *in vitro*.
20. The method of claim 19, wherein the antibody is detectably labeled.
21. The method of claim 20, wherein the label is selected from the group consisting of a radioisotope, a fluorescent compound, a bioluminescent compound, a chemoluminescent compound and an enzyme.
22. A method of treating a cell proliferative disorder associated with expression of GDF-7, comprising contacting the cells with a reagent which suppresses the GDF-7 activity.
23. The method of claim 22, wherein the reagent is an anti-GDF-7 antibody.

24. The method of claim 22, wherein the reagent is a GDF-7 antisense sequence.
25. The method of claim 22, wherein the cell is a neural cell.
26. The method of claim 22, wherein the reagent which suppresses GDF-7 activity is introduced to a cell using a vector.
27. The method of claim 26, wherein the vector is a colloidal dispersion system.
28. The method of claim 27, wherein the colloidal dispersion system is a liposome.
29. The method of claim 28, wherein the liposome is essentially target specific.
30. The method of claim 29, wherein the liposome is anatomically targeted.
31. The method of claim 30, wherein the liposome is mechanistically targeted.
32. The method of claim 31, wherein the mechanistic targeting is passive.
33. The method of claim 31, wherein the mechanistic targeting is active.
34. The method of claim 33, wherein the liposome is actively targeted by coupling with a moiety selected from the group consisting of a sugar, a glycolipid, and a protein.

35. The method of claim 34, wherein the protein moiety is an antibody.
36. The method of claim 35, wherein the vector is a virus.
37. The method of claim 36, wherein the virus is an RNA virus.
38. The method of claim 37, wherein the RNA virus is a retrovirus.
39. The method of claim 38, wherein the retrovirus is essentially target specific.
40. The method of claim 39, wherein the moiety for target specificity is encoded by a polynucleotide inserted into the retroviral genome.
41. The method of claim 40, wherein the moiety for target specificity is selected from the group consisting of a sugar, a glycolipid, and a protein.
42. The method of claim 41, wherein the protein is an antibody.



14.5 day fetal brain

16.5 day fetal brain

2 day neonatal brain

7 day neonatal brain

NB41 neuroblastoma

Neuro 2A neuroblastoma

muscle

yeast tRNA



FIG. I

1 GCTGCAGAGCCGCCACCGGTACCCAGGACCAGGCGCTGGGTACGCAAGCCAACCTGGGC 60
 A G S R K A N L G
 61 GGTGCGAGGCGGCGGACTGCGCTGGCTGGGACTCGGGGAGCGCAGGGAAGCGGTGGT 120
 G R R R R T A L A G T R G A Q G S G G
 121 GCGGCGGTGGCGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGAGGC 180
 G G G G G G G G G G G G G G G G G G A G
 181 AGGGGCCACGGGCGCAGAGGCCGGAGCCGCTGCAGTCGCAAGTCACTGCACGTGGACTTT 240
 R G H G R G R G R S R C S R K S L H V D F
 241 AAGGAGCTGGGCTGGGACGACTGGATCATCGCGCCATTAGACTACGAGGCATACCACTGC 300
 K E L G W D D W I I A P L D Y E A Y H C
 301 GAGGGCGTTTGGGACTTTCCTCTGCGCTCGCACCTGGAGCCTACCAACCACGCCATCATT 360
 E G V C D F P L R S H L E P T N H A I I
 361 CAGACGCTGCTCAACTCCATGGCGCCCGACGCTGCGCCAGCCTCCTGCTGCGTGCCCGCA 420
 Q T L L N S M A P D A A P A S C C V P A
 421 AGGCTCAGTCCCATCAGCATTTCTCTACATCGATGCCGCCAACAAACGTGCTACAAGCAG 480
 R L S P I S I L Y I D A A N N V V Y K Q
 481 TACGAAGACATGGTGGTGGAGGCCCTGCGGCTGCAGGTAG 519
 Y E D M V V E A C G C R *

FIG.2

GDF-7 GGGGAGRGHGRGRSRCSRKSLHVDF-KELGWDDWIIAPLDYEAHYHCEGVCDPFLRSHLEP----

GDF-1 RPRRDAEPVLGGPGGACARRLLVVSF-REVGWHRWVIAPRGFLANYCQGQCALPVALSGSGGPP

BMP-2 REKRQAKHKQRKRLKSSCKRHPLYVDF-SDVGWNDWIVAPPYHAFYCHGECPPFLADHLNS----

BMP-4 KRSPKHHSQRARKKNKNCRRHSLVDF-SDVGWNDWIVAPPYHAFYCHGDCPPFLADHLNS----

Vgr-1 SRGSGSDYNGSELKTACKKHELVSF-QDLGWQDWIIAPKGYAANYCDGECSPFLNAHMNA----

OP-1 LRMANVAENSSDQRACKKHELVSF-RDLGWQDWIIAPEGYAAYCEGECAPFLNSYMNA----

BMP-5 SRMSSVGDYNTSEKQACKKHELVSF-RDLGWQDWIIAPEGYAAYCDGECSPFLNAHMNA----

BMP-3 EQTLKKARRKQWIEPRNCARRYLKVDF-ADIGWSEWIIIPKSFDAYYCSGACQFPMPSLKPSS----

MIS GPGRQRSAGATAADGPCALRELSVDL-----RAERSVLIPETYQANNCGVCGWPQSDRNPRY----

Inhibin α ALRLLRPPPEEPAAHANCHRVALNISF-QELGWERWIVPPSFIHYCHGGCGLHIPNLSLPV-

Inhibin β A HRRRRRGLECDGKV-NICKKQFFVSF-KDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSL-

Inhibin β B HRIKRGLECDGRT-NLCRCRQFFIDF-RLIGWNDWIIAPTGYGNYCEGSCPAYLAGVPGSAS-

TGF- β 1 HRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWK-WIHEPKGYHANFCLGPCPYIWSLD-----

TGF- β 2 KKRALDAAYCFRNVDNCCLRPLYIDFRKDLGWK-WIHEPKGYANFCAAGACPYLWSSD-----

TGF- β 3 KKRALDTNYCFRNLEENCVRPLYIDFRQDLGWK-WVHEPKGYANFCSGCPYLRSDA-----

GDF-7 -TNHAI IQTLNS--MAPDAAPASCCV--PARLSPISILYI-DAANNVVYKQYEDMVVEACGGCR

GDF-1 ALNHAVLRALMHA--AAPGAADLPCCV--PARLSPISVLFF-DNSDNNVVLQYEDMVVDECGCR

BMP-2 -TNHAI VQTLVNS---VNSKIPKACCV--PTELSAISMLYL-DENEKVVLKNYQDMVVEGCGCR

BMP-4 -TNHAI VQTLVNS---VNSSIPKACCV--PTELSAISMLYL-DEYDKVVLKNYQEMVVEGCGCR

Vgr-1 -TNHAI VQTLVHL--MNPEYVPKPCCA--PTKLNAISVLVF-DDNSNVILKKYRNMVVRACGCH

OP-1 -TNHAI VQTLVHF--INPETVPKPCCA--PTQLNAISVLVF-DDSSNVILKKYRNMVVRACGCH

BMP-5 -TNHAI VQTLVHL--MFPDHVPKPCCA--PTKLNAISVLVF-DDSSNVILKKYRNMVVRACGCH

BMP-3 --NHATIQSIVRA-VGVVPGIPEPCV--PEKMSSLSILFF-DENKNVVLKVYPMNTVESACGR

MIS -GNHVVL LLMQA--RGAA LARPPCV--PTAYAGKLLISLSEER--ISAHHVPMNVATECGCR

Inhibin α -PGAPPTPAQPYS-----LLPGAQPCCAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQHACAI

Inhibin β A -SFHSTVINHYMRGHSFANLKSCV--PTKL RPSMLYY-DDGQNI IKKDIQNMIVEECGCS

Inhibin β B -SFHTAVVNGYMRGLNPGT-VNSCQI--PTKLSTMSMLYF-DDEYNIVKRDVPNMIVEECGCA

TGF- β 1 -TQYSKVLALYNQ--HNPGASAAPCCV--PQALEPLPIVYY-VGRKPKV-EQLSNMIVRSCKCS

TGF- β 2 -TQHSRVLSLYNT--INPEASASPCV--SQDLEPLTILYY-IGKTPKI-EQLSNMIVKSCKCS


TGF- β 3 -TTHSTVLGLYNT--LNPEASASPCV--PQDLEPLTILYY-VGRTPKV-EQLSNMIVKSCKCS

FIG. 3

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FIG. 4

[illegible]

A. CLASSIFICATION OF SUBJECT MATTER IPC(5) : A61K 37/36; C12P 13/06; C12N 1/22, 15/18, 15/66; C07K 15/28 US CL : 530/399, 388.23; 435/69.1, 69.4, 320.1, 252.3; 536/23.5 According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 530/399, 388.23; 435/69.1, 69.4, 320.1, 252.3; 536/23.5 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) APS, DIALOG, Genbank, PIR, SwissPro search terms; growth differentiation factor-7 SEQ ID NOS. 5 and 6		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	MOLECULAR ENDOCRINOLOGY, Volume 6, Number 11, issued 1992, Jones et al., "Isolation of Vgr-2, a Novel Member of the Transforming Growth Factor-beta-Related Gene Family", pages 1961-1968.	1-42
A	MOLECULAR ENDOCRINOLOGY, Volume 4, Number 7, issued 1990, Lee, "Identification of a Novel Member (GDF-1) of the Transforming Growth Factor-beta Superfamily", pages 1034-1040.	1-42
A	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES USA, Volume 88, issued May 1991, Lee, "Expression of growth/differentiation factor 1 in the nervous system: Conservation of a bicistronic structure", pages 4250-4254.	1-42
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C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	THE JOURNAL OF BIOLOGICAL CHEMISTRY, Volume 268, Number 5, issued 15 February 1993, McPherron et al., "GDF-3 and GDF-9: Two New Members of the Transforming Growth Factor-beta Superfamily Containing a Novel Pattern of Cysteines", pages 3444-3449.	1-42

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